

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

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#9.
Bill
2-23-d 1635

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,663

DATE: 02/16/2001
TIME: 16:36:30

Input Set : A:\B0045591.txt
Output Set: N:\CRF3\02162001\I530663.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Chiang, Vincent Lee C.
5 Tsai, Chung-Jui
6 Hu, Wen-Jing
8 <120> TITLE OF INVENTION: GENETIC ENGINEERING OF LIGNIN BIOSYNTHESIS IN PLANTS
10 <130> FILE REFERENCE: 66040-9651
12 <140> CURRENT APPLICATION NUMBER: 09/530,663
13 <141> CURRENT FILING DATE: 2000-07-11
15 <150> PRIOR APPLICATION NUMBER: PCT/US98/24138
16 <151> PRIOR FILING DATE: 1998-11-12
18 <150> PRIOR APPLICATION NUMBER: 08/969,046
19 <151> PRIOR FILING DATE: 1997-11-12
21 <160> NUMBER OF SEQ ID NOS: 17
23 <170> SOFTWARE: Word 97 (DOS text format)

ERRORED SEQUENCES

562 <210> SEQ ID NO: 9
563 <211> LENGTH: 31
564 <212> TYPE: DNA
565 <213> ORGANISM: Populus tremuloides Michx. (aspen)
567 <400> SEQUENCE: 9
E--> 568 ttggatccgg (i)adaciggi ytticciaarg g 31
570 <210> SEQ ID NO: 10
571 <211> LENGTH: 28
572 <212> TYPE: DNA
573 <213> ORGANISM: Populus tremuloides Michx. (aspen)
575 <400> SEQUENCE: 10
E--> 576 ttggatccgt (i)gdcparcar gtgaggg same error 28
578 <210> SEQ ID NO: 11
579 <211> LENGTH: 27
580 <212> TYPE: DNA
581 <213> ORGANISM: Populus tremuloides Michx. (aspen)
583 <400> SEQUENCE: 11
E--> 584 atgtcgac (i)ckdatrcada tytcacc same 27
628 <210> SEQ ID NO: 17
629 <211> LENGTH: 11
630 <212> TYPE: DNA
631 <213> ORGANISM: Populus tremuloides Michx. (aspen)
633 <400> SEQUENCE: 17
634 tctcaccaac c 11
E--> 640 1
E--> 643 2 delete at end of file

"i" is invalid in the
sequence itself-use "n,"
instead,
and explain
in 2207-22237
section

VERIFICATION SUMMARY DATE: 02/16/2001
PATENT APPLICATION: US/09/530,663 TIME: 16:36:31

Input Set : A:\B0045591.txt
Output Set: N:\CRF3\02162001\I530663.raw

L:568 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:576 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:584 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:640 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:11 SEQ:17
M:254 Repeated in SeqNo=17